

Fig. 1A

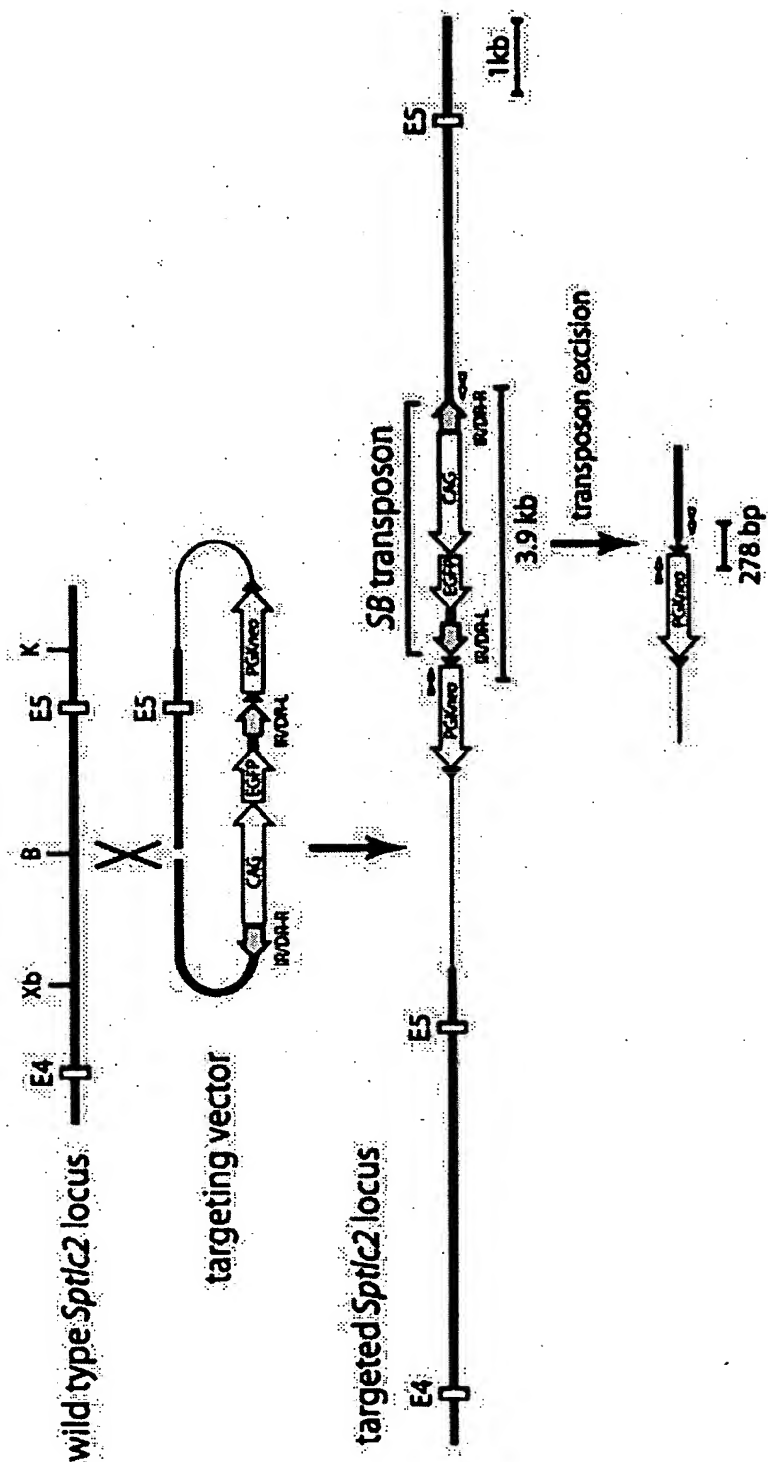


Fig. 1B

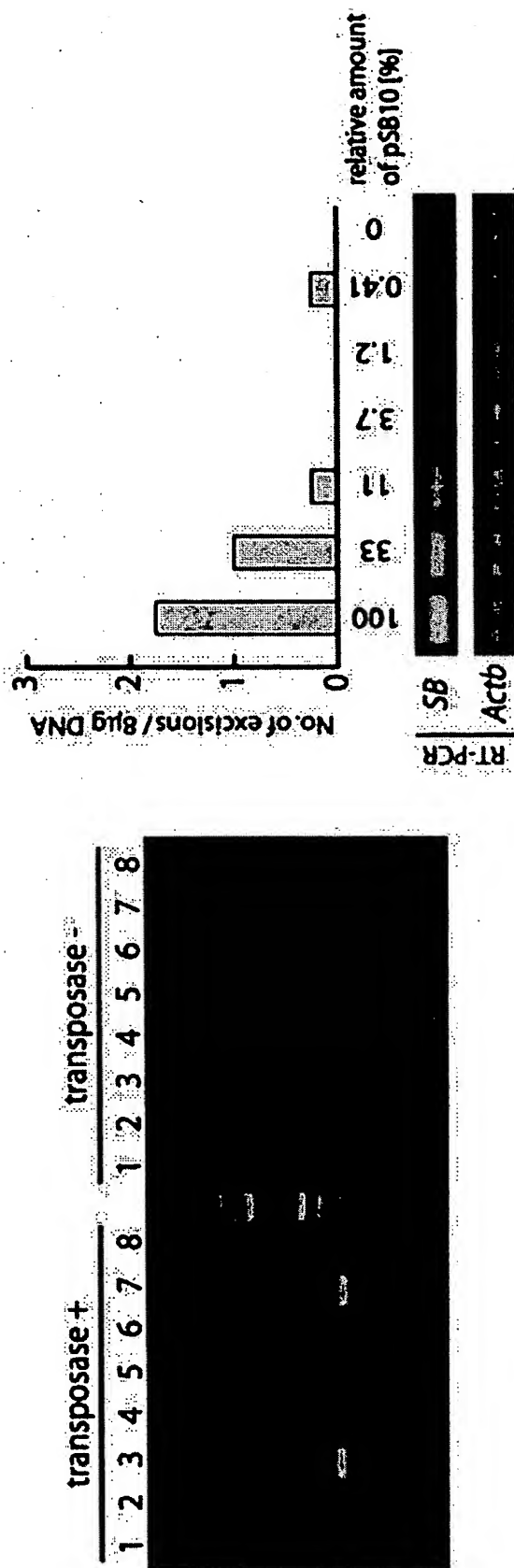


Fig. 1C

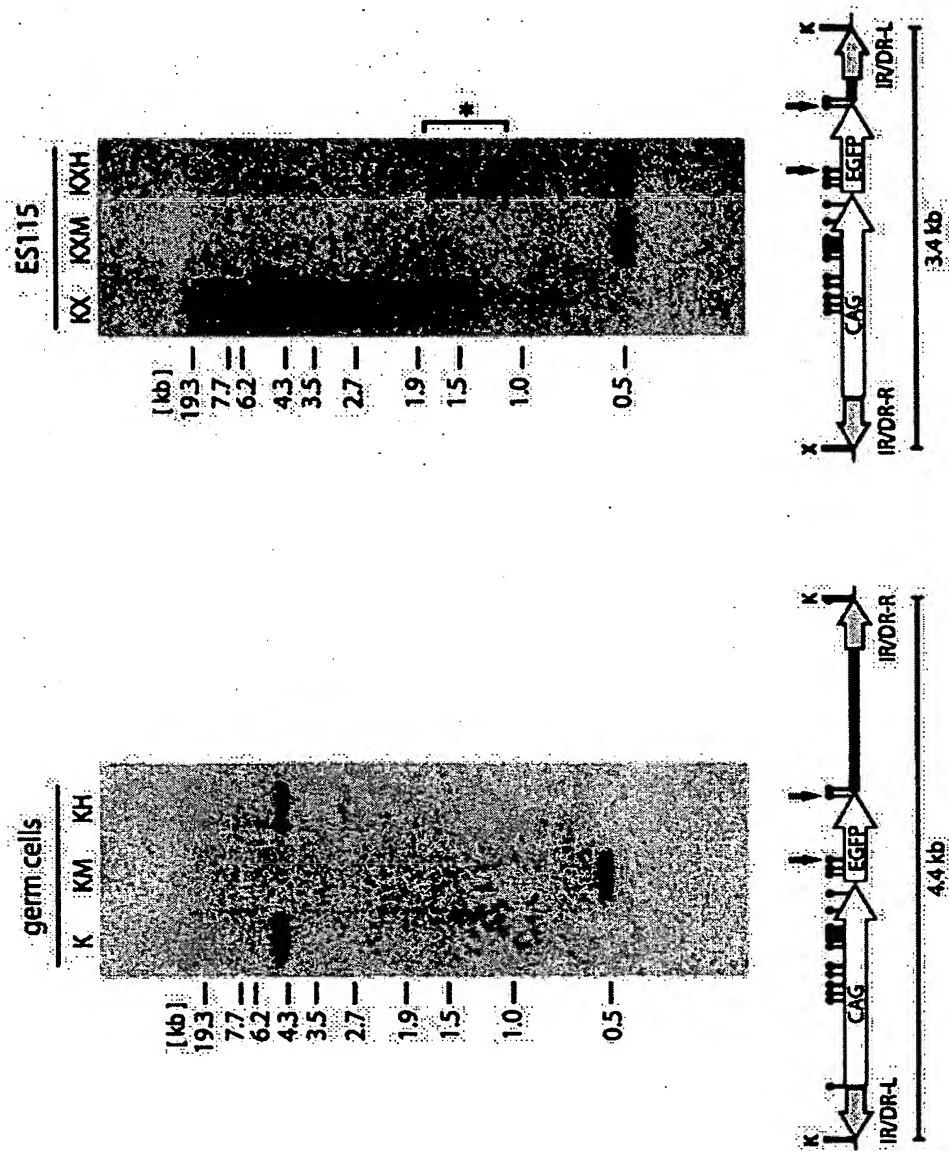


Fig. 1D

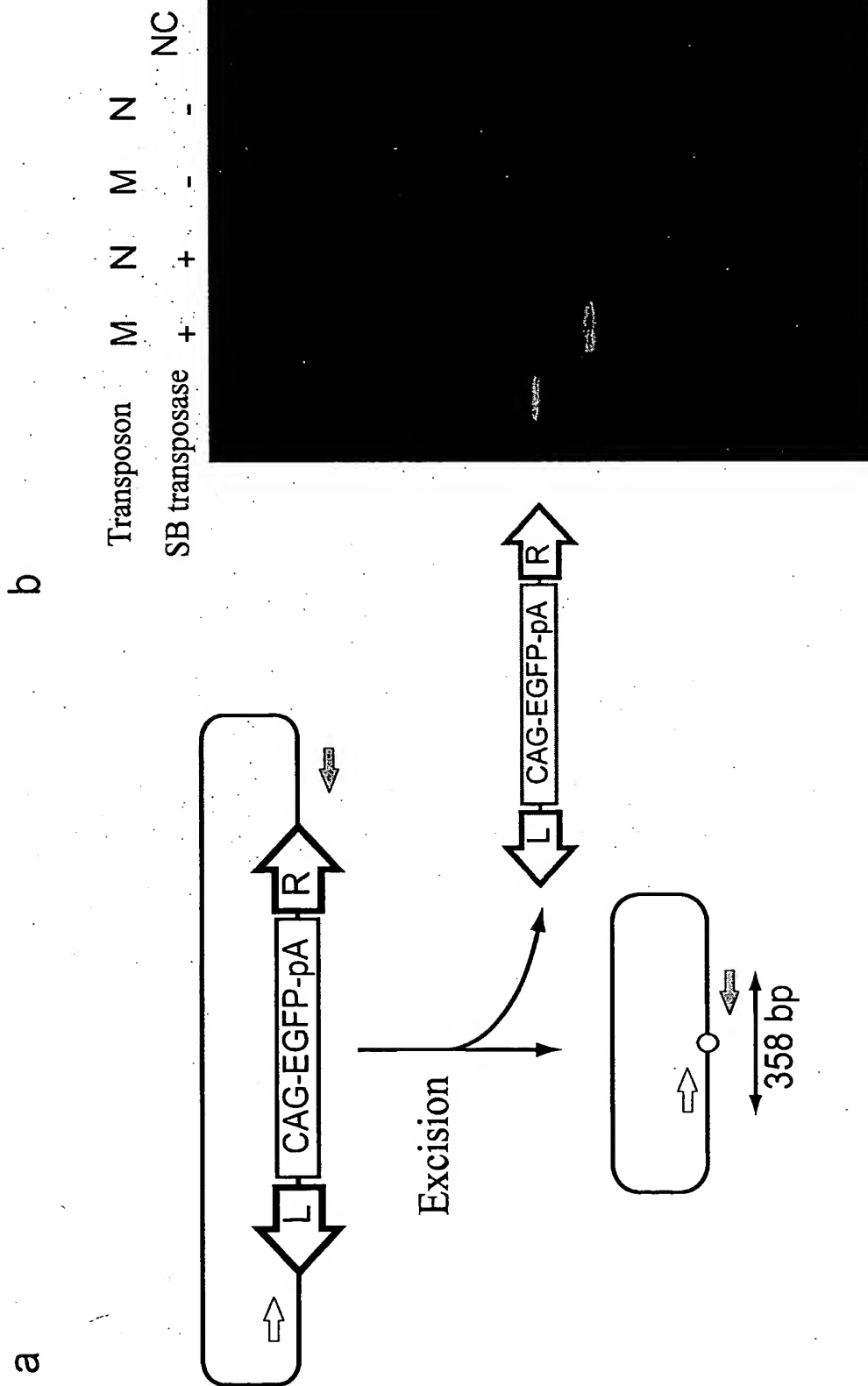


Fig. 2A

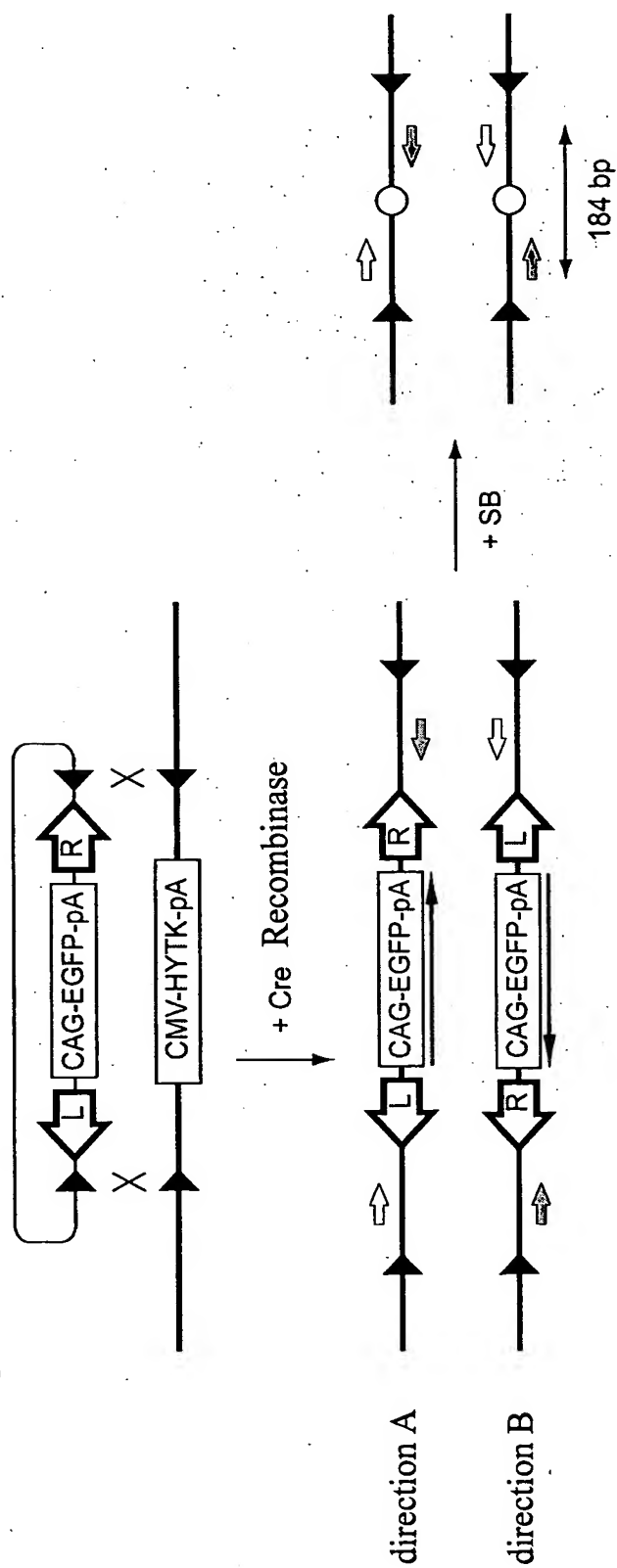
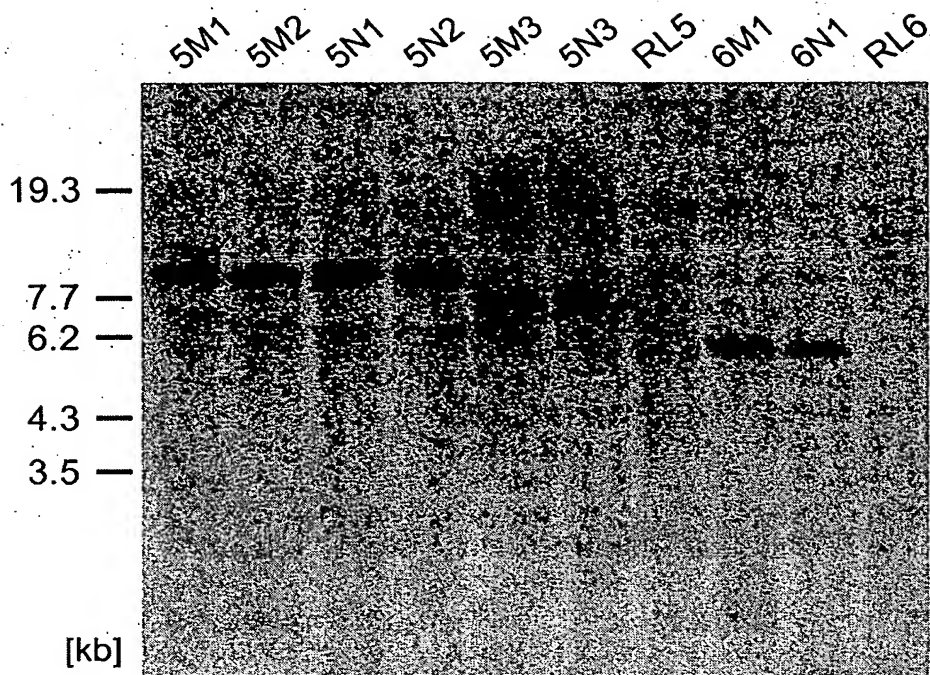


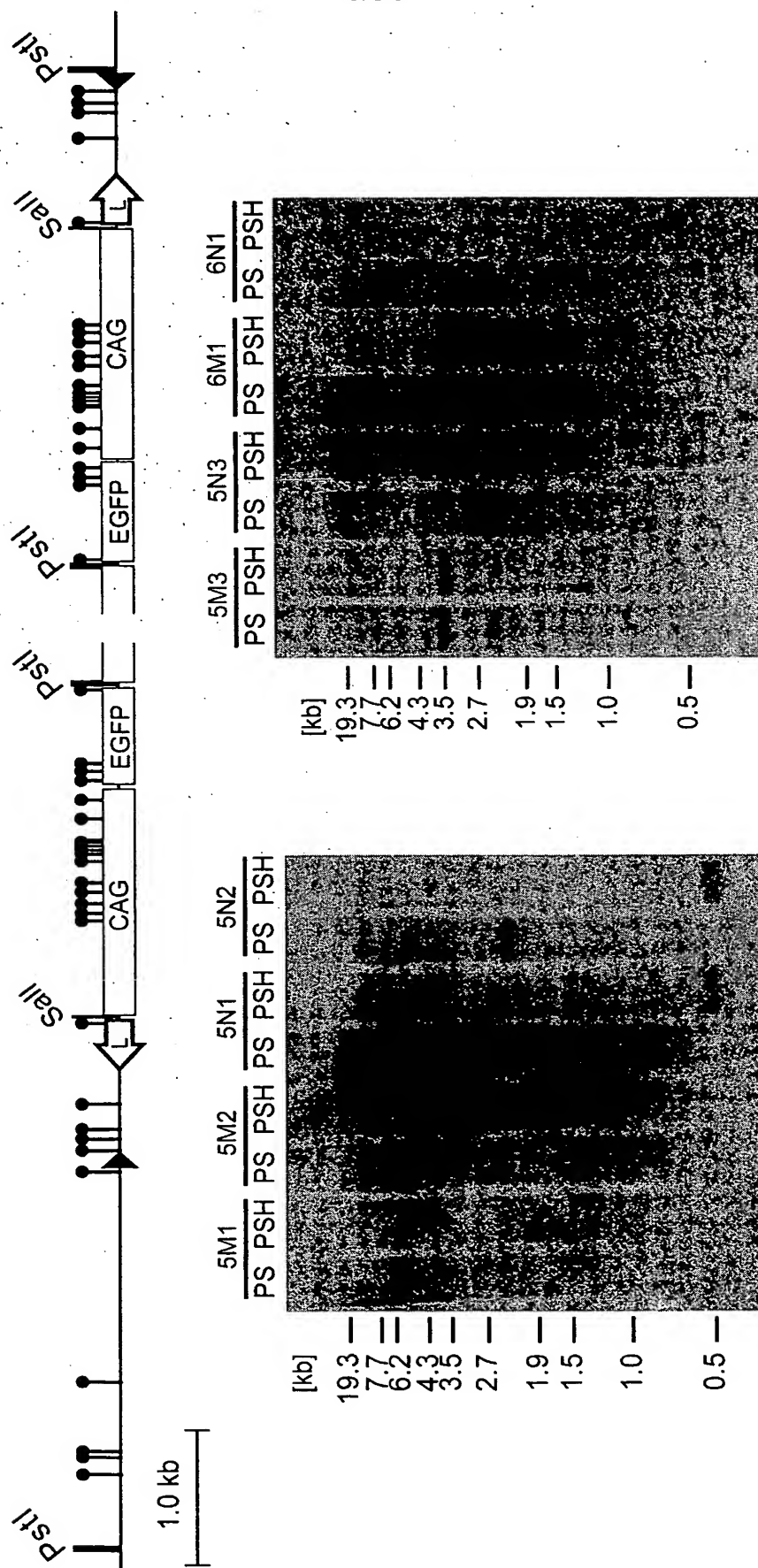
Fig. 2B



RL5- direction A



Fig. 2D



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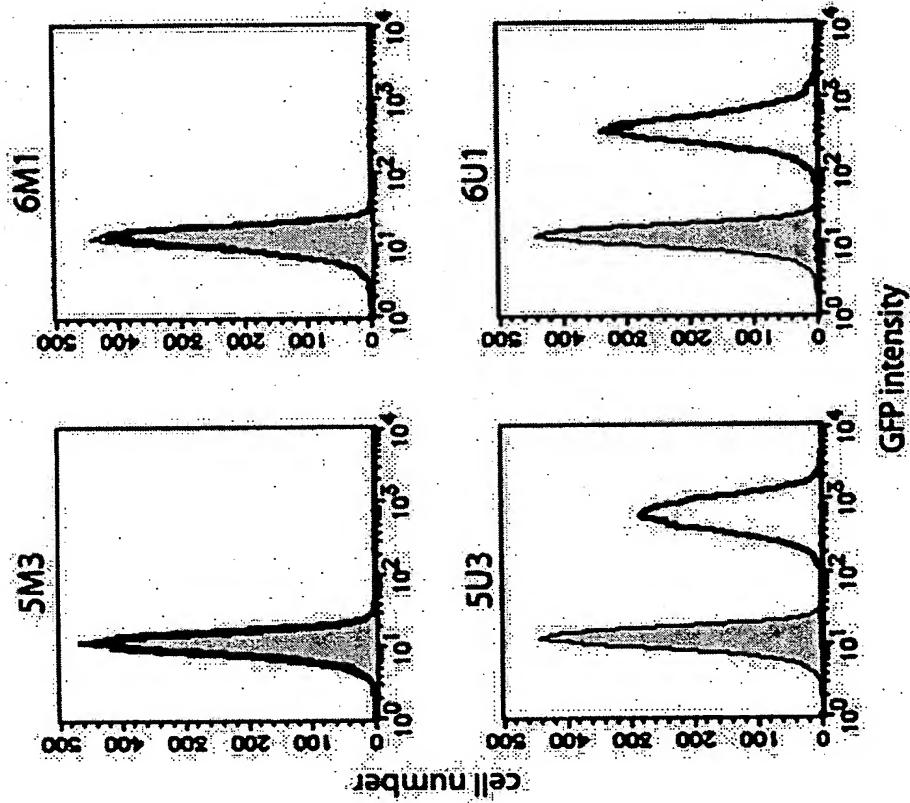


Fig. 2E

	M	1	2	3	4	5	6	7	8	9	10	M	NC	M	Methylation
5M1														+	
5M2														+	
5M3														+	
5N1														-	
5N2														-	
5N3														-	
6M1														+	
6N1														-	

1 μ g template											parental done			
M	1	2	3	4	5	6	7	8	9	10		M		
5M1	[Gel Image]										NC	M	+	RLS
5M2	[Gel Image]										NC	M	+	RLS
5U1	[Gel Image]										NC	M	-	RLS
5U2	[Gel Image]										NC	M	-	RLS

	1 μ g template											10 ng template											$m^{15}CpG$	parental clone
	M	1	2	3	4	5	6	7	8	9	10	M	1	2	3	4	5	6	7	8	9	10		
5M3																							+	RL5
5U3																							-	RL5
6M1																							+	RL6
6U1																							-	RL6

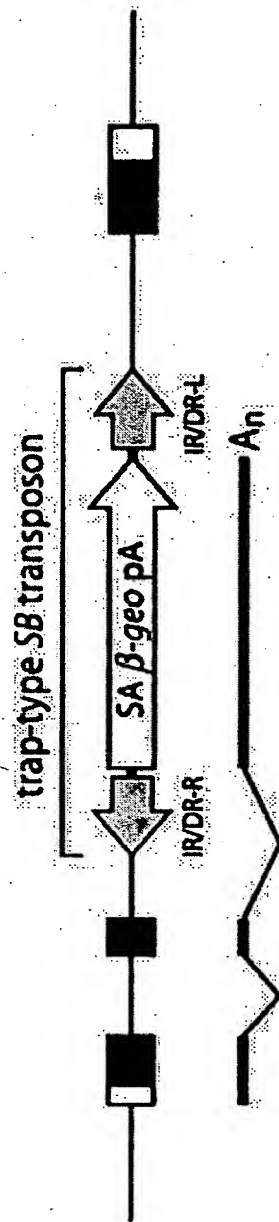


Fig. 4A

Fig. 4B

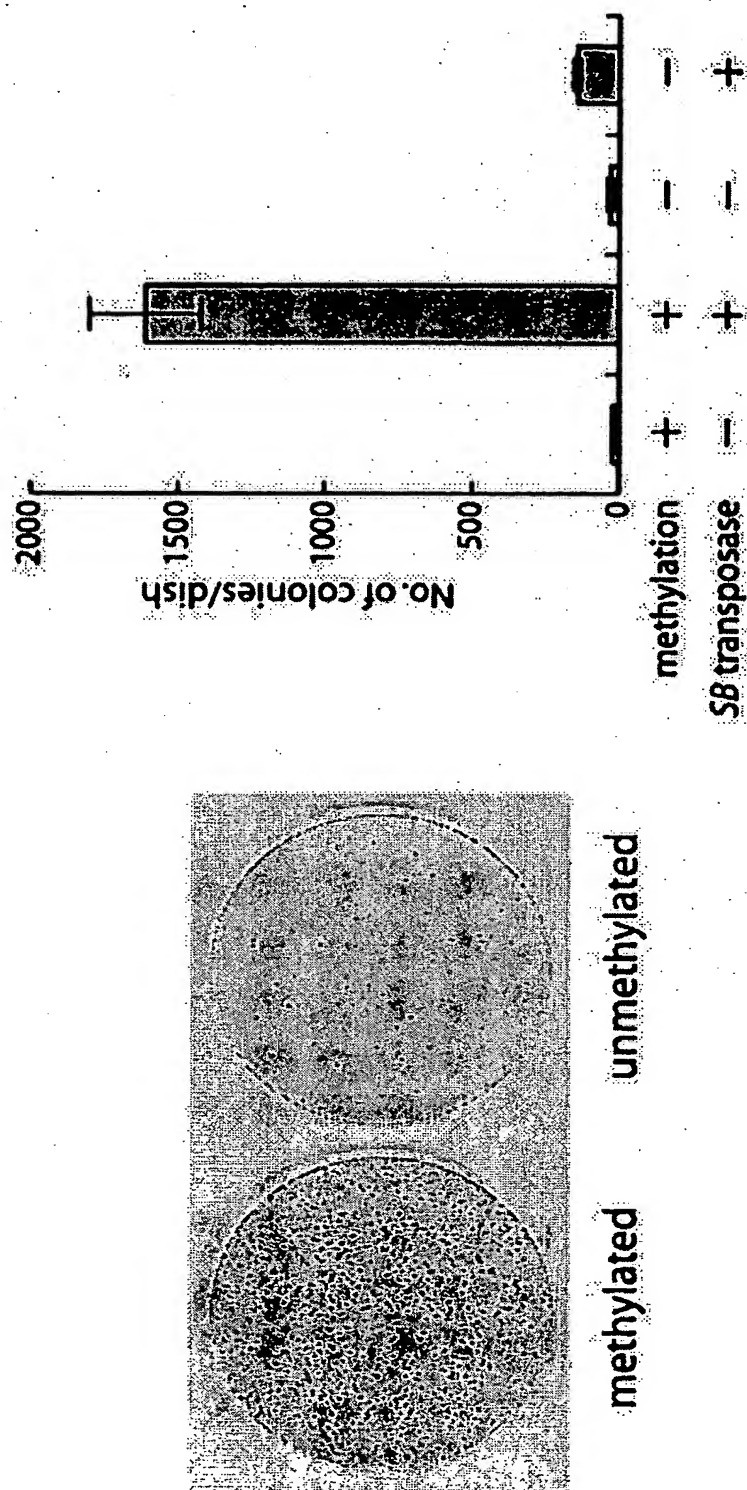
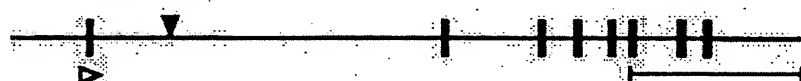


Fig. 4C

M1: Chr. 10, NM_172508



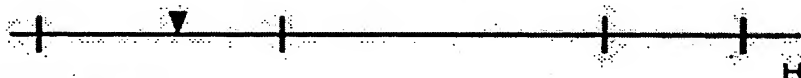
M2S: Chr. 7, ENSMUST49387



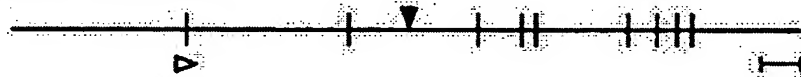
M2L: Chr. 8, ENSMUSESTT33450



M3: Chr. 16, ENSMUSESTT27446



M4: Chr. 19, Pten



N1: Chr. 1, ENSMUST27914



N6: Chr. 16, ENSMUSESTT26711

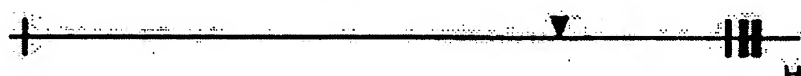


Fig. 4D

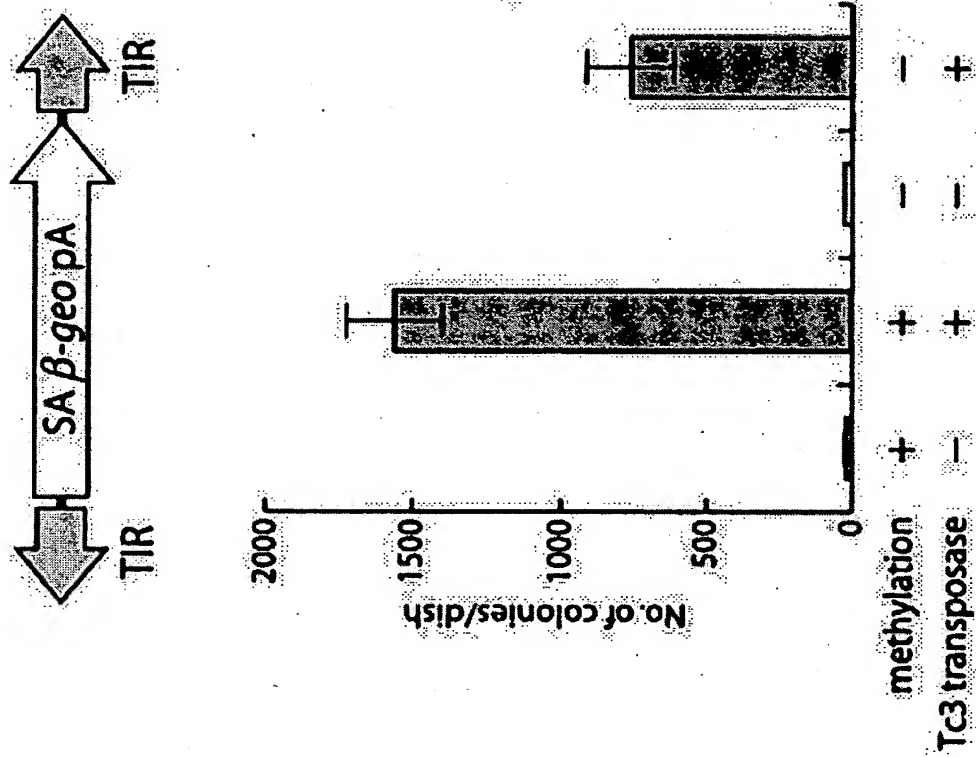


Fig. 5A

CLUSTAL W (1.81) Multiple Sequence Alignments

Sequence type explicitly set to DNA
Sequence format is Pearson
Sequence 1: X01005 1610 bp
Sequence 2: Z29098 1773 bp
Sequence 3: Z29102 1717 bp
Sequence 4: U11641 1263 bp
Sequence 5: U11652 1296 bp
Sequence 6: L48685 1455 bp
Start of Pairwise alignments
Aligning...
Sequences (5:6) Aligned. Score: 3
Sequences (3:4) Aligned. Score: 3
Sequences (1:2) Aligned. Score: 9
Sequences (3:5) Aligned. Score: 3
Sequences (4:5) Aligned. Score: 95
Sequences (1:3) Aligned. Score: 9
Sequences (3:6) Aligned. Score: 10
Sequences (4:6) Aligned. Score: 3
Sequences (1:4) Aligned. Score: 1
Sequences (2:3) Aligned. Score: 99
Sequences (1:5) Aligned. Score: 3
Sequences (2:4) Aligned. Score: 3
Sequences (1:6) Aligned. Score: 2
Sequences (2:5) Aligned. Score: 3
Sequences (2:6) Aligned. Score: 10
Guide tree file created: [clustalw.dnd]
Start of Multiple Alignment
There are 5 groups
Aligning...
Group 1: Sequences: 2 Score:32613
Group 2: Delayed
Group 3: Delayed
Group 4: Sequences: 2 Score:22721
Group 5: Sequences: 4 Score:12095
Sequence:6 Score:13071
Sequence:1 Score:12960
Alignment Score 47622
CLUSTAL-Alignment file created [clustalw.aln]
CLUSTAL W (1.81) multiple sequence alignment:

Z29098	CGAGCCCCAACCACCTATTAATTCGAACAGCATGTTTTTTTGCAGTGC6CAATGTTTAAC
Z29102	_____TAAC
U11641	_____
U11652	_____
L48685	_____
X01005	_____

Z29098	ACACTATATTATCAATACTACTAAAGATAACACATACCAATGCATTTCTCTCAAAAGAGA
Z29102	ACACTATATTATCAATACTACTAAAGATAACACATACCAATGCATTTCTCTCAAAAGAGA
U11641	_____
U11652	_____

Fig. 5B

L48685
X01005
CAGTTGAAGTC—GGAAG
CAGTGCTGGCCAAAAAGA

Z29098
Z29102
U11641
U11652
L48685
X01005
ATTTTATTCTCTTCACGACGAAAAAAAAGTTTGTCTATTTCCAACAACAACAAAAAT
ATTTTATTCTCTTCACGACGAAAAAAAAGTTTGTCTATTTCCAACAACAACAAAAAT
TTTACATACACTTAAGTTGAGTCATTAAA—ACTCGTTTTTCAACTACACCACAAAT
TATCCA—CTTTTGGTTTTTGTGTATA—CTTTTTCTCAAGCATCCATTGAC

Z29098
Z29102
U11641
U11652
L48685
X01005
ATGAGTAATTTATTCAAACGGTTTGTCTAAGAGATAAGAAAAAGTGACCACTATTAATT
ATGAGTAATTTATTCAAACGGTTTGTCTAAGAGATAAGAAAAAGTGACCACTATTAATT
AACATGT
ATTAGGT
TTC—TTGTTAA—CAAACAAT—AGTTTTGGCAAGTCAGTTAGGACATCTACTT
TTG—AATTTTTCCGTGTGCATAAAGCGAAATGTTACGCAAAATTTGCGGACCAA—ACAT
* *

Z29098
Z29102
U11641
U11652
L48685
X01005
CGAACGCGGCGTAAGCTTACCTTAATCTCAAGAAGAGCAAAACAAAAGCAACTAATGTAA
CGAACGCGGCGTAAGCTTACCTTAATCTCAAGAAGAGCAAAACAAAAGCAACTAATGTAA
TGGCTG—ATAAGTCC—CGGGTTTGACAC—TAGTATTAATGCA—
TGGCTG—ATAAGTCC—CGGGTTTGACACATAGATGGCTCGCTAGTATTAATGCA—
TGTGATGACACAAGT—CATTTTTCCAACAATTGT—TTACAGACAGATTATTTCA
TACATGATTATCGATTTTTCTGAATTTTATTCAATTT—TTGATTTTTCTGTTTTCC
* * * *

Z29098
Z29102
U11641
U11652
L48685
X01005
CGGAATCATTATCTAGTTATGATCTGCAATAAT—GTCACAATACAGCATGCAAAAA
CGGAATCATTATCTAGTTATGATCTGCAATAAT—GTCACAATACAGCATGCAAAAA
TATTATTTTATATAGGACCAACCTTCAAATGATTCGTGTCAAAATTTGACSTC
TATTATTTTATATAGTACCAACCTTCAAATGATTCGTGTCAAAATTTGACSTCTGTAG
CTTATAATTCAGTGTATCACAAT—CCAGTGG—GTCAGAAATTTACATACA—
AATTTTCATTATTTTTTTGAATTTATCAATAAACGCACTCTGTTTGTGCACTGG—A
* * * * *

Z29098
Z29102
U11641
U11652
L48685
X01005
AATTTTAGATTGCTGCA—GATCAGTAGAAGTTTAGCAACGATGGTTCGTGGTAAACCTA
AATTTTAGATTGCTGCA—GATCAGTAGAAGTTTAGCAACGATGGTTCGTGGTAAACCTA
—AATTAGTTTGTGAGA—GCAACTTTTGTATTGTGAAGAAAA
TCAATTAGTTTGTGAGATAGAGCGTCTTTTGTGAAGCAACTTTTGTATTGTGAAGAAAA
—CTAAGTTGACTGTG—CCTTAAA—CAGCTTGGAAAAATTCAG—AAATGA
TTTGTGTTGGTGAATAAT—TATTTTAAAGGTATGGTAAATCTGTTGGGTGTAAAAATC
* * * * *

Z29098
Z29102
U11641
U11652
L48685
X01005
TTTCTAAAG—AAATCAGAGTATTGATTAGGGATTATTTTAAATCTGGAAG
TTTCTAAAG—AAATCAGAGTATTGATTAGGGATTATTTTAAATCTGGAAG
TGGAAAAAATTTCAATTCGAATTCGTGTTTTGATAAAATACTGTTTTCTGAAGGGAAAA
TGGAAAAA—AGGAATTTCTGTTTTGATAAAATACTGTTTTCTGAAGGGAAAA
TGTGATGGC—TTTGAAGCTTC—TGATAGACTAATGACATCATTGAG
TTTCTTGG—ACGTCAAGAAAGCCATTGTAG—CTGGCTTCAACAAGGAAT
* * * * *

Z29098
Z29102
U11641
U11652
L48685
X01005
ACACTTACGGAGATAAGCAAGCAATTAATTTGCCAAGTCGTCTGTGCATGGGGTGAAT
ACACTTACGGAGATAAGCAAGCAATTAATTTGCCAAGTCGTCTGTGCATGGGGTGAAT
AA—TGGGGTGG—AAGCAAAAAGTTGGCTTGATAATGATTTCCGGAAGTCTGCCCAA—
AA—TACAGTGG—AAGCAAAAAGTTGGCTTGATAATGATTTCCGGAAGTCTGCCCAA—
TCAATT—GGAGGTGACCTGTGGATGATTT—CAAGGCTACCTTCA—AACGCAAT—
ACCCACGAAAAGCTCGCGCTGCAAAATCAACGTTCTCCGTGCACTATTTGGAAGTAATC

Fig. 5C

* *

Z29098 ACAAATTTTCAAAAAA-AATG66AATATTGAAAAATAA-CA-TT6CGAATAGAGGCCGAA
Z29102 ACAAATTTTCAAAAAA-AATG66AATATTGAAAAATAA-CA-TT6CGAATAGAGGCCGAA
U11641 GGAAATCAATAATAATTGATTG6TATGCAAAATTCAAGCG-AGGTGAAATGAGCACGGA
U11652 GGAAATCAACAATAATTGATTG6TATGCAAAATTCAAGCG-TG6TGAAATGAGCACGGA
L48685 GCCTCTTGCTTGACATAATG6GAAAAATCAAAAGAAATCAGCCAAACCATGGGACCAG
X01005 AAGAAGTACCAAACTGAGGTGABTTGAAAAATATTATTTTAAATAAAATGTTTAGA
* * ** *

Z29098 CATCAGCAA-TAACACCCCGCAGCAAAAAGACAA-CTGGCCAAAATTGTTAAGGCTGAT
Z29102 CATCAGCAA-TAACACCCCGCAGCAAAAAGACAA-CTGGCCAAAATTGTTAAGGCTGAT
U11641 GGACGGTGA-ACGCASTGGACGCCGAAAG-AG-6TGGTTACCGACGAAAA-
U11652 GGACGGTGA-ACGCASTGGACGCCGAAAG-AG-6TGGTTACCGACGAAAA-
L48685 CAGCCGTCA-TACGCTCAGGAATGAGACGCATTCTGTCTCTAGAGATAAA-
X01005 AATCCGTGCTTTGAGAATCTGCGCCGCGACGGCT-CGAGTACAACCCATAGGATGGAT
* * *

Z29098 CGTCGCCAATCTTTGAGAAATTTGGCTTCTAAGTGGTCGCA-GCAATTGGCAAAACT
Z29102 CGTCGCCAATCTTTGAGAAATTTGGCTTCTAAGTGGTCGCA-GCAATTGGCAAAACT
U11641 CATCAAAAAATCCACAAAAT-GATTTTGAATGACCGTAAAAAGAASTTGAATCSAGAT
U11652 CATCAAAAAATCCACAAAAT-GATTTTGAATGACCGTAAAAAGAASTTGAATCSAGAT
L48685 CAT-ACTGTGGTGGCAAAAGT-GCAATCAATCCGAGAACGACAGCAAAAGGACCT
X01005 CGC-AACATCCTCCGATCAGCA-AGAGAAGATCCGATAG-GACCGCCACGGATAT
* * *

Z29098 GTCAAGCBAGAGTGGACGCGACAAATTAAGATAT-TGGATATGTTTTTATAAAGT
Z29102 GTCAAGCBAGAGTGGACGCGACAAATTAAGATAT-TGGATATGTTTTTATAAAGT
U11641 AACAAA-GGCTTTAAACATATCAAA-GGAACGTGT-TGGTCATATCATTATCAAA-
U11652 AGCAGA-GGCTTTAAAGATATCAAA-GGAACGTGT-TGGTCATATCATTATCAAA-
L48685 TGTGAA-GATGCTGGAGAAAACAGGTATGAATGTTTCTATATCCACAGTAAAAACGAGTC
X01005 -TCAATGATTATAAGTTCTCCAAATGAACCTGTAC-CAAGTAAACGAACTGTTCTGTC
* * ** *

Z29098 ATGTTTTGTTATTACCTGTGCATCGTACCCAATAACTTACTCGTAATCTTACTGTAAGG
Z29102 ATGTTTTGTTATTACCTGTGCATCGTACCCAATAACTTACTCGTAATCTTACTGTAAGG
U11641 -TATTTGGATAT-GCGGAAGCTCTGTGCAAAATG66TGCCGCGCBACTCAGAT-TTGAC
U11652 -TATTTGGATAT-GCGGAAGCTCTGTGCAAAATG66TGCCGCGCBACTCAGAT-TTGAC
L48685 CTATATCSACATAACCTGAAAGGC-CGCTCAGCAAGGAAGAGCCA-CTGCTCCAAAAC
X01005 GACGTTTACAGCAAGCAGGACTACACGGACGA-AAGCCAGTCAAGAAACGTTTATCAGT
* *

Z29098 CAAGG-AAAAACCTTGCTTACGCTTCGTCAAAAAAAGAGCGTTTGCAATGGG-CTCG
Z29102 CAAGG-AAAAACCTTGCTTACGCTTCGTCAAAAAAAGAGCGTTTGCAATGGG-CTCG
U11641 CAAAA-ACAACAACGTGTTGATGATTCT-GAGCGGTGTTTGAGGCTGT-TAAC
U11652 CAAAA-ACAACAACGTGTTGATGATTCT-GAGCGGTGTTTGAGGCTGT-TAAC
L48685 CCGCATAAAAAGCCAGACTACGTTTGCAACTGCACATGGGACAAATATGTTACTTTT
X01005 AAGAA-AAATCGCATG6CTCGA6TTGCGTGGGCAAAAGC-GCATCTTCTGTTGGGACGTC
* * *

Z29098 G6AAAGGATGTCTTGACTCAAAGGCAATG66ATACCATCATATTGAGGATGAAGCTAA
Z29102 G6AAAGGATGTCTTGACTCAAAGGCAATG66ATACCATCATATTGAGGATGAAGCTAA
U11641 TCGTAATACACCCAGTTTTTCCGTCGATATG-TAAGATG6ATGAAACATGGCTCCATC
U11652 TCGTAATACACCCAGTTTTTCCGTCGATATG-TGACAATG6ATGAAACATGGCTCCATC
L48685 TGGAGAAATGCTCTCTCTGTTGCTGATGAA-AAAAAATGAACTATTTGGCCAT
X01005 A6GAATG6GCTAAACACATCTGTTGACGAA-A6CAAGTTCAATTTGTTG66GAGT
* * *

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Fig. 5D

Z29098 ATTTGATGTTAGTGTGCGCGATACGAGAAAACGCTCATCCGTAAAGAGGTCAGAAACATA
Z29102 ATTTGATGTTAGTGTGCGCGATACGAGAAAACGCTCATCCGTAAAGAGGTCAGAAACATA
U11641 ACTACACTCCTGAGTTCBATCAACAGTCGCTGAGTGGACAGCAGCCGCT—GAACCGTC
U11652 ACTACACTCCTGAGTTCBAACAGTCGCTGAGTGGACAGCAGCCGCT—GAACCGTC
L48685 AATGACCATCCTTAT—GTTTGGAGGAAAAAGGGGAGCTTSCAAGCCG—AAGATCA
X01005 GATGGAATTCCTG—GGTACGTCCTCTGTTGGCTCTAGGTACTCTCCAAAGTA
* * *

Z29098 CCATAAAGACTGCCTTAAAAGAACAAAGTTTCTGCGAGCACTATGATGAGGATG
Z29102 CCATAAAGACTGCCTTAAAAGAACAAAGTTTCTGCGAGCACTATGATGAGGATG
U11641 TCCGAAG—CGTGGAAAGACTCAAAAGTCCGCTGGCAAAGTAATGGCTCTGTTTT
U11652 TCCGAAG—CGTGGAAAGACTCAAAAGTCCGCTGGCAAAGTAATGGCTCTGTTTT
L48685 CCATC—CCAAGCGTGAAGCAGCGGGG—TGGCAGCATCATGTTGTGGGGTG
X01005 TCAATGC—CCAACCGTTAAGCATGGAGG—TGGGAGCCTCATGGTGTGGGGTG
* * * * *

Z29098 TATGCTGCGAAAGGATTAGGAAAACCTTCATTTCATTGAAGGGACAGTTAATGCTGAAAA
Z29102 TATGCTGCGAAAGGATTAGGAAAACCTTCATTTCATTGAAGGGACAGTTAATGCTGAAAA
U11641 TTGGAAATGCGCATGGAATAATTTTATCGATTATCTTGAGAAAGGAAAAACCATCAACAG
U11652 TTTCGATGCGCATGGAATAATTTTATCGATTATCTTGAGAAAGGAAAAACCATCAACAG
L48685 CTTTGCTGCAAGGAGGACTGGTGCACCTCACAAAATAGATGGCATCATGACAAAAGAAAA
X01005 CTTACCCAGCACTTCATGGGCCCACTAAGGAGAAATCCAAAGCATTATGGATCGTTTTCA
* * *

Z29098 ATATATTAATATTTTACAAGATAGTTTGTGCGCATCAATACCAAACTATTAGATTGCGG
Z29102 ATATATTAATATTTTACAAGATAGTTTGTGCGCATCAATACCAAACTATTAGATTGCGG
U11641 —TGACTATTATATGGCTTATTGTAGCGTTTGAAGGTCGAAATCGCGGCAAAATGG
U11652 —TGACTATTATATGGCTTATTGTAGCGTTTGAAGGTCGAAATCGCGGCAAAACGG
L48685 TTATGTGGCTATATTGAAGCAACATCTCAAGACATCAGTCAGGAAAGTTCAAGCTTGGTCA
X01005 ATACGAAAACATCTTTGAACTACAATGCGACCTGGGCACCTCAAAATGTGGGCCGTGG
* * *

Z29098 TGAATTCAGTTTTAGCAGGACGGAGCATCATCGCAC—ACAGCCAAGCGAACCAAAA
Z29102 TGAATTCAGTTTTAGCAGGACGGAGCATCATCGCAC—ACAGCCAAGCGAACCAAAA
U11641 —CCCCATATGAGAAAGAAAAAGTGTGTTCCGACCAAGCAATGCACCGTGGCCAAA
U11652 —CCCCATATGAGAAAGAAAAAGTGTGTTCCGACCAAGCAACGACCGTGGCCAAA
L48685 CAAATGGGTCTTCCAAATGGCAATGACCTCAAGCAT—ACTTCCAAAGTTGTGGCAA
X01005 C—TTCGTGTTTCAAGGAGGATAACGATCCTAAGCAT—ACTTCTCTCATGTGCGTT
* * * * *

Z29098 ATTGGCTGCAATATAATCAAATGGAAGTTTTAGATTGGCCATCAAATAGTCCAGATCTAA
Z29102 ATTGGCTGCAATATAATCAAATGGAAGTTTTAGATTGGCCATCAAATAGTCCAGATCTAA
U11641 GTCAGTAAGAACGATGGCAAA—AATTCATGAATTGGGCTTCGAAATGCTTCCCCACCC
U11652 GTCATTGAGAACGATGGCAAA—AATTCATGAATTGGGCTTCGAAATGCTTCCCCACCC
L48685 AATGGCTTAAGGTCAACAAAGTCAAGGTATTGGAGTGGCCATCACAAAGCTGTGACCTCA
X01005 CATGGTTTCAAGCTGCTCATGTGCAATTGCTGATTTGGCCAAAGTCAGTCTCCGAGTTGA
* * * * *

Z29098 GCCCAATTGAAAAATATTTGGTGGCTAATGAAAAACAGCTT—CGAAAT—GAGCC—ACA
Z29102 GCCCAATTGAAAAATATTTGGTGGCTAATGAAAAACAGCTT—CGAAAT—GAGCC—ACA
U11641 ACTATATTCTCCAGATCTGGCCCGCAGCGAATTTTCTTGT—TCTCA—GACCT—CAA
U11652 ACCGTATTCTCCAGATCTGGCCCGCAGCGAATTTTCTTGT—TCTCA—GACCT—CAA
L48685 ATCCTATAGAAAAGGAGGAATGAGCCAAATTCACCCAACTTATTGTGG—AAGCTTGTG
X01005 ATCCAATAGAGCATTTGTGGGAAGAGTTGGAAGAGCTCTTGGAGGTATTGCGGCT—TCA
* * *

Z29098 AAGGAATATTTCTGACTTGAAAAATCAAGTTGCAAGAGATGTGGGACTCAATTTCTCAAGA
Z29102 AAGGAATATTTCTGACTTGAAAAATCAAGTTGCAAGAGATGTGGGACTCAATTTCTCAAGA

Fig. 5E

U11641 AAGGATGCTCGCAGGGAAAAAATTGGCTGCAATGAA-----GAGG
U11652 AAGG-ATGCTCGCAGGGAAAAAATTGGCTGCAATGAA-----GAGG
L48685 GAAGGCTACTCGAAATGTTTGACCCAAGTTAAACAATTT-----AAAG
X01005 AATGCAGATGCCAAATTC-AACCAAGTTGAAAAACGCTTGAAAGCTATCCCATGTCA
* * * * *

Z29098 GCATTGCAAAAATTTGTTAAGCTCAATGCCAAAACGAGTTAAATGCGTAATGCAGGCCAA
Z29102 GCATTGCAAAAATTTGTTAAGCTCAATGCCAAAACGAGTTAAATGCGTAATGCAGGCCAA
U11641 TAATCGCCBAAAC-TAAGGCCTATTTTGAGGCAAAACCGTAAGAGTACTA-----CCA
U11652 TGATCGCCBAAAC-TGAGGCCTATTTTGAGGCAAAACCGAAGGAGTACTA-----CCA
L48685 GCAATGCTA-----CCAAATACTAATTAAGTGTATGTTAACTTC-TGACCCA-CTGG
X01005 GTTATTCACAAGCTGATCGA-CTCGATGCCACGTCGTTGTCAAGCTGTTATTGATGCAAA
* * * * *

Z29098 GGGCGACGTTACACAATTCTAATATTAATTAAATTATTGTTTTAAGTATGATAGTAAATC
Z29102 GGGCGACGTTACACAATTCTAATATTAATTAAATTATTGTTTTAAGTATGATAGTAAATC
U11641 AAATGGTATCAAAAAATTGGAAGGTCGTTATAATCGTGGTATCGCTCTTGA-AGGGGACT
U11652 AAATGGTATCAAAAAATTGGAAGGTCGTTATAATCGTGGTATCGCTCTTGA-AGGGGACT
L48685 GAATGTGATGAAAGAAATAAAGCTGAAATGAATCATTCTCTACTATTATTCTG-----
X01005 CGGATACGCGACAAAGTATTAAGCATAATTATGTTGT-TTTTAAATCCAATTGC-TC
* * * * *

Z29098 ACATTACGCCCGCTTCGAATTAATAGTGGTCACCTTTTTCTTATCTCTTAAGCAAACCGT
Z29102 ACATTACGCCCGCTTCGAATTAATAGTGGTCACCTTTTTCTTATCTCTTAAGCAAACCGT
U11641 ATGTTGAATAATAA-AAACGAATTTTGACAAAAAA-TGTGTTTTCTTTGTTAGACCGG
U11652 ATGTTGAATAATAA-AAACGAATTTTGACAAAAAAATGTTTTCTTTGTTAGACCGG
L48685 ATATTTACATTTCTTAAATAAA-GTGGTGA-TCCTAAGTACCTTAAGACAGGGAAT
X01005 ATATTCGGTACTT-----TAATTGTCATTTCTTGCAACCTCGGTTTTTCAATATTT
* * * * *

Z29098 TTGAATAAATTACTCATATTTTTGTTGTTGTTGGAAATAGAGCAAACTTTTTTTTCGT
Z29102 TTGAATAAATTACTCATATTTTTGTTGTTGTTGGAAATAGAGCAAACTTTTTTTTCGT
U11641 -GGACTTATCAGCCAACCTGTTA-----
U11652 -GGACTTATCAGCCAACCTGTTA-----
L48685 C-TTACTCGGATTAATGTCAGGAATTGTGAAAAAGTGAAGTTAAATGTAATTTG-GC
X01005 C-TAGTTTTTCGATTTTTTTGAATTTTTCTGAAGTTTTTCAAAATCTGTTGAACAT
* * * * *

Z29098 CBTGAAGAGAATAAAATTCTCTTTGAGACGAAATGCATTGGTATGTGTTATCTTTAGTAG
Z29102 CBTGAAGAGAATAAAATTCTCTTTGAGACGAAATGCATTGGTATGTGTTATCTTTAGTAG
U11641 -----
U11652 -----
L48685 TAAGGTGTATGTAACCTTCGACTTCAACTG-----
X01005 TTTTG-ATGAATATTGTGTTTTAGATTTTGTGAACACTGTGTTGAAGTTTCAAAACA
* * * * *

Z29098 TATTGATAATATAGTGTGTTAAACATTGCGCACTGCAAAAAAACATGCTGTTCGAATTA
Z29102 TATTGATAATATAGTGTGTTAAACATTGCGCACTGCAAAAAAACATGCTGTTCGAATTA
U11641 -----
U11652 -----
L48685 -----
X01005 AAATAACCACTTAGAAAAAAGTTACACACAAAAAACCAAAAGTGGATATCTTTTGGCCA
* * * * *

Z29098 ATAGTGGTTGGGGCTCG
Z29102 ATAGTGGTTGGGGCTCG
U11641 -----
U11652 -----

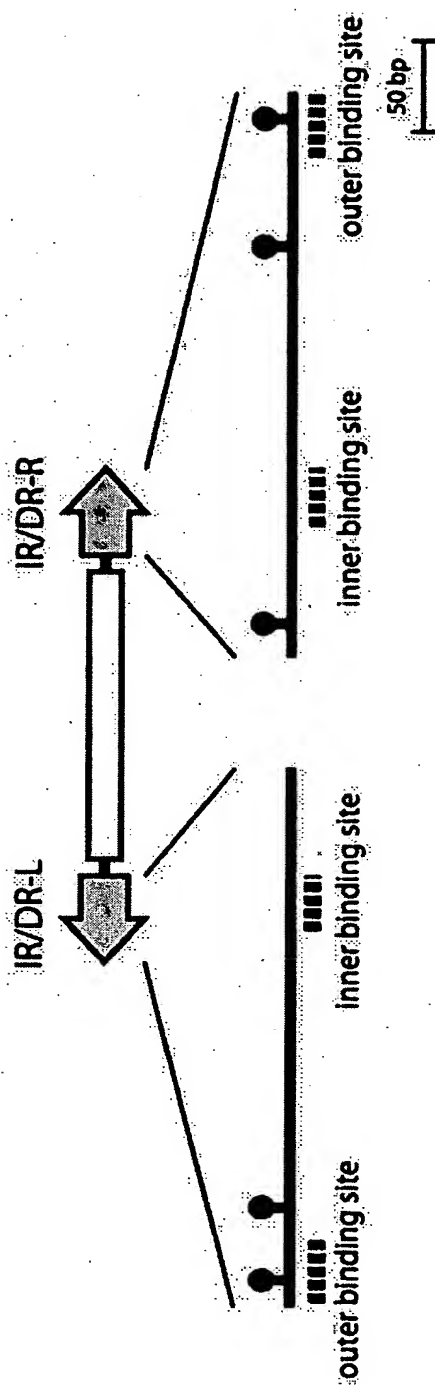
Fig. 5F

L48685
X01005

GCAC78

(
(
X01005:0.47463,
(
U11641:0.02397,
U11652:0.01879)
:0.47911)
:0.01531,
(
Z29098:0.00029,
Z29102:0.00029)
:0.42978,
L48685:0.46683):

Fig. 6A



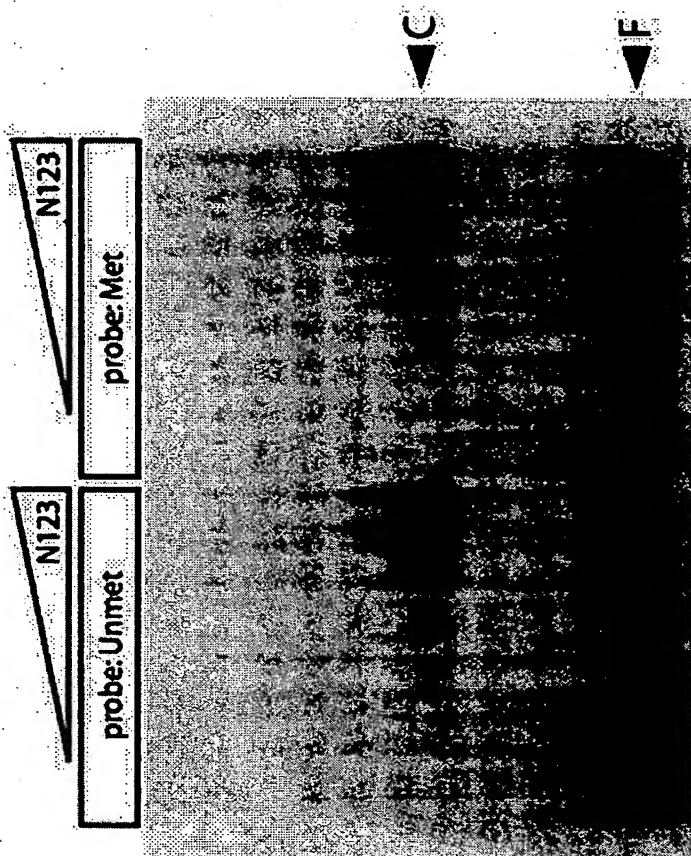


Fig. 6B

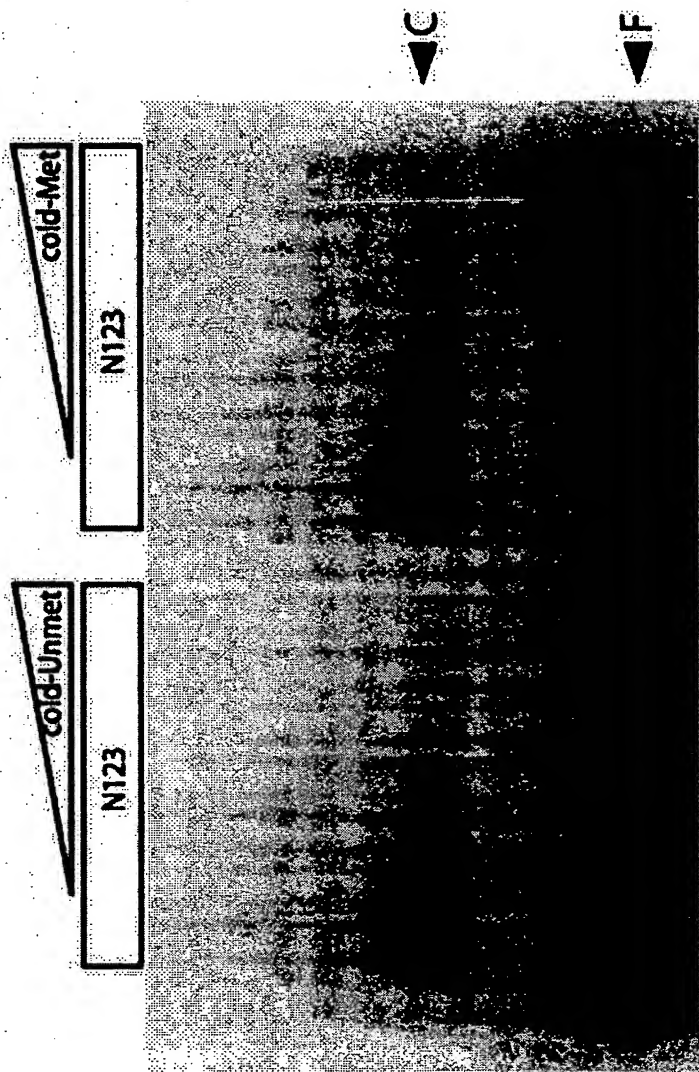


Fig. 6C

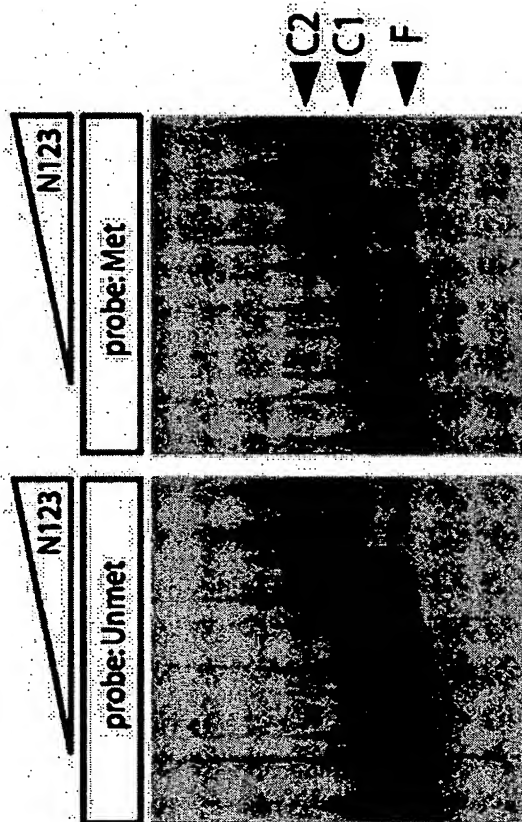


Fig. 6D

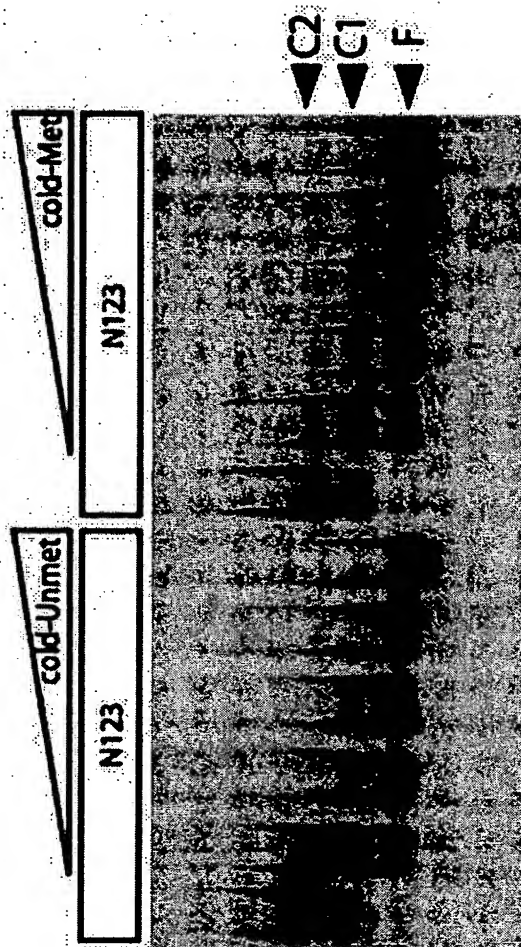
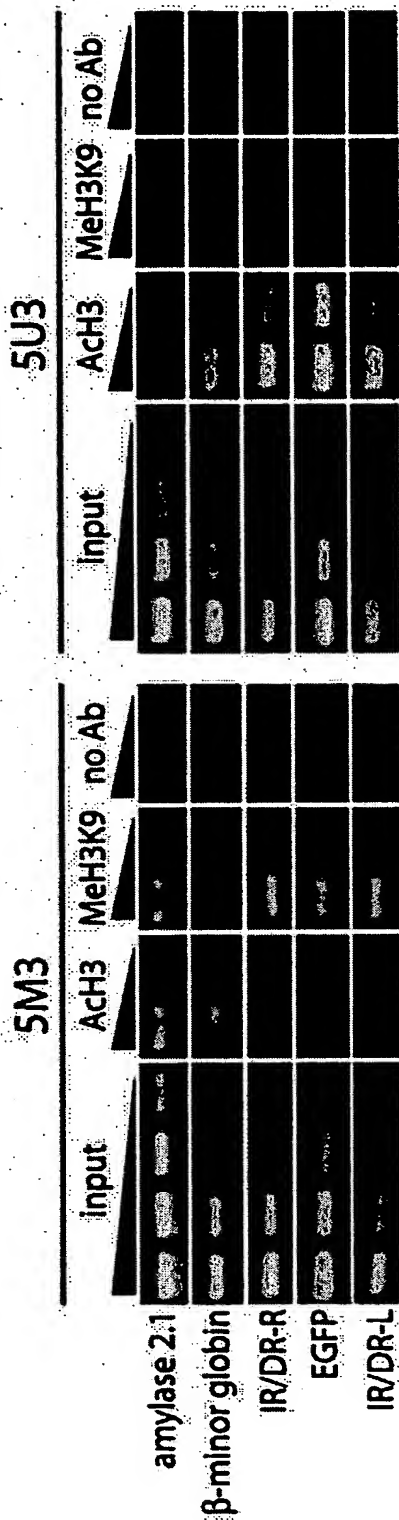


Fig. 6E



Fig. 7A

Fig. 7B



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